****
Reviewer Comments:
<210>   70
<211>   174
<212>   PRT
<213>   Oerskovia jenensis

<400>   70
(ERRORED PORTION SHOWN BELOW)

Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala

          115   120   125

Please remove the blank lines between the above amino acid numbers and
their respective amino acids: amino acid numbers must appear directly
below their amino acids.

<210>   125
<211>   189
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   consensus sequence

(ERRORED PORTION SHOWN BELOW)

<220>

```
<221>  VARIANT
<222>  1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71, 81,
87, 89, 93, 109-111, 113, 116
<223>  Xaa can be any naturally occurring amino acid
```

The above "<222>" line exceeds the Sequence Rules' required 72-character line limit; please insert a hard return after "69-71,"; that way, the remaining response will move to the next line. See below for sample:

```
<220>
<221>  VARIANT
<222>  1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71,
       81, 87, 89, 93, 109-111, 113, 116
<223>  Xaa can be any naturally occurring amino acid



<210>  134
<211>  340
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic

<400>  134
```

(ERRORED PORTION SHOWN BELOW)

Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His


```
     50                      55                      60
```

Please remove the blank lines between the above amino acid numbers and their respective amino acids. Amino acid numbers must appear directly below their amino acids.


```
<210>  639
<211>  255
<212>  PRT
```

<213> Streptogrisin C

Regarding the above "<213> Streptogrisin": per Sequence Rules, the only valid "<213>" responses are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require an explanation in the "<220>-<223>" section; please clearly indicate the source of the genetic material. "Streptogrisin" also appears in subsequent sequences (as the "<213>" response).

<210>   640
<211>   185
<212>   PRT
<213>   Streptogrisin B

<400>   640

(see below)

Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly

                 20   25   30

Please check the above "<213>" response: as indicated in Sequence 639 above, the only valid "<213>" responses are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the "<220>-<223>" section. Please remove the blank lines between the above amino acid numbers and their respective amino acids; amino acid numbers must appear directly below their amino acids.

<210>   642
<211>   188
<212>   PRT
<213>   Streptogrisin D

<400>   642

(see below)

```
Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val His Asp Gly


            100                 105                 110
```

Please check "Streptogrisin" as the above "<213>" response. Please
remove the blank lines between the above amino acid numbers and their
amino acids. Amino acid numbers must appear directly below their amino
acids.

To correct the sequence listing errors noted in this report - The
recommended method for correction of errors is to access the sequence
listing working file using the software program in which the listing was
originally prepared, e.g., the project file in PatentIn, make any
necessary corrections within that program, then generate a new sequence
listing file. Use of a word processing program to correct errors
directly in the original sequence listing file is strongly discouraged,
since such programs often introduce unintended changes to the sequence
listing, rendering the listing unacceptable. When the working file or
original program is not available for correction, then use of a common
or plain text-only editor, such as NotePad, to edit the original
sequence listing file may suffice.

```
*************************************************************
```

Application No: 10576331   Version No: 2.0

Input Set:

Output Set:

Started: 2012-01-24 13:57:36.425
Finished: 2012-01-24 13:57:58.381
Elapsed: 0 hr(s) 0 min(s) 21 sec(s) 956 ms
Total Warnings: 605
Total Errors: 28
No. of SeqIDs Defined: 656
Actual SeqID Count: 656

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)

```
             Input Set:


            Output Set:



          Started:   2012-01-24 13:57:36.425
         Finished:   2012-01-24 13:57:58.381
          Elapsed:   0 hr(s) 0 min(s) 21 sec(s) 956 ms
   Total Warnings:   605
     Total Errors:   28
No. of SeqIDs Defined:   656
 Actual SeqID Count:   656
```

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (45)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (61)
W 402	Undefined organism found in <213> in SEQ ID (62)
W 402	Undefined organism found in <213> in SEQ ID (65)
W 402	Undefined organism found in <213> in SEQ ID (66)
W 402	Undefined organism found in <213> in SEQ ID (69)
	This error has occured more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (70)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81)
W 213	Artificial or Unknown found in <213> in SEQ ID (82)
W 213	Artificial or Unknown found in <213> in SEQ ID (83)
W 213	Artificial or Unknown found in <213> in SEQ ID (84)

```
                     Input Set:


                     Output Set:



               Started:    2012-01-24 13:57:36.425
              Finished:    2012-01-24 13:57:58.381
               Elapsed:    0 hr(s) 0 min(s) 21 sec(s) 956 ms
        Total Warnings:    605
          Total Errors:    28
  No. of SeqIDs Defined:    656
     Actual SeqID Count:    656


Error code      Error Description


E   341       'Xaa' position not defined   SEQID (125)   POS (170)

E   341       'Xaa' position not defined   SEQID (125)   POS (171)

E   341       'Xaa' position not defined   SEQID (125)   POS (172)

E   341       'Xaa' position not defined   SEQID (125)   POS (173)

E   341       'Xaa' position not defined   SEQID (125)   POS (174)

E   341       'Xaa' position not defined   SEQID (125)   POS (175)

E   341       'Xaa' position not defined   SEQID (125)   POS (176)

E   341       'Xaa' position not defined   SEQID (125)   POS (177)

E   341       'Xaa' position not defined   SEQID (125)   POS (178)

E   341       'Xaa' position not defined   SEQID (125)   POS (179)

E   341       'Xaa' position not defined   SEQID (125)   POS (180)

E   341       'Xaa' position not defined   SEQID (125)   POS (181)

E   341       'Xaa' position not defined   SEQID (125)   POS (182)

E   341       'Xaa' position not defined   SEQID (125)   POS (183)

E   341       'Xaa' position not defined   SEQID (125)   POS (184)

E   341       'Xaa' position not defined   SEQID (125)   POS (185)

E   341       'Xaa' position not defined   SEQID (125)   POS (186)

E   341       'Xaa' position not defined   SEQID (125)   POS (187)

E   341       'Xaa' position not defined   SEQID (125)   POS (188)

E   341       'Xaa' position not defined   SEQID (125)   POS (189)
              This error has occured more than 20 times, will not be displayed

E   355       Empty lines found between the amino acid numbering and the

E   321       No. of Bases conflict, this line has no nucleotides  SEQID (134)
```

```
           Input Set:


           Output Set:



           Started:    2012-01-24 13:57:36.425
          Finished:    2012-01-24 13:57:58.381
           Elapsed:    0 hr(s) 0 min(s) 21 sec(s) 956 ms
   Total Warnings:    605
     Total Errors:    28
No. of SeqIDs Defined:    656
  Actual SeqID Count:    656
```

Error code   Error Description

E   355   Empty lines found between the amino acid numbering and the

E   321   No. of Bases conflict, this line has no nucleotides SEQID (640)

E   355   Empty lines found between the amino acid numbering and the

E   321   No. of Bases conflict, this line has no nucleotides SEQID (642)

<110>   Jones, Brian E.
         Kolkman, Marc
         Leeflang, Chris
         Oh, Hiroshi
         Poulose, A.J.
         Sadlowski, Eugene S.
         Shaw, Andrew
         van der Kleij, Wilhelmus A.H.
         van Marrenwijk, Leo

<120>   Serine Proteases, Nucleic Acids Encoding Serine Enzymes and
         Vectors and Host Cells Incorporating Same

<130>   GC819-2-US/B

<140>   10576331
<141>   2012-01-24

<150>   PCT/US2004/039066
<151>   2004-11-19

<150>   US 60/523,609
<151>   2003-11-19

<160>   656

<170>   PatentIn version 3.2

<210>   1
<211>   1680
<212>   DNA
<213>   Cellulomonas strain 69B4

<400>   1
gcgcgctgcg cccacgacga cgccgtccgc cgttcgccgg cgtacctgcg ttggctcacc   60
acccaccaga tcgacctcca taacgaggcc gtatgaccag aaagggatct gccaccgccc   120
accagcacgc tcctaacctc cgagcaccgg cgaccgccgg gtgcgatgaa agggacgaac   180
cgagatgaca ccacgcacag tcacgcgggc cctggccgtg ccaccgcag ccgccacact   240
cctggcaggc ggcatggccg cccaggccaa cgagcccgca ccacccggga gcgcgagcgc   300
accgccacgc ctggccgaga agctcgaccc cgacctcctc gaggccatgg agcgcgacct   360
gggcctcgac gcggaggaag ccgccgccac cctggcgttc agcacgacg cagccgagac   420
cggcgaggcc ctcgccgaag agctcgacga ggacttcgcc ggcacctggg tcgaggacga   480
cgtcctgtac gtcgccacca ccgacgagga cgccgtcgag gaggtcgagg cgaaggcgc   540
cacgccgtc accgtcgagc actccctggc cgacctcgag gcctggaaga ccgtcctcga   600
cgccgccctc gagggccacg acgacgtgcc cacctggtac gtcgacgtcc cgaccaacag   660
cgtcgtcgtc gccgtcaagg ccggagccca ggacgtcgcc gccggcctcg tcgaaggtgc   720
cgacgtcccg tccgacgccg tgaccttcgt cgagaccgac gagacccgc ggaccatgtt   780
cgacgtgatc ggcggcaacg cctacaccat cggggggcgc agccgctgct cgatcgggtt   840
cgcggtcaac ggcgggttca tcaccgccgg ccactgcggc cgcaccggcg ccaccaccgc   900
caaccccacc gggaccttcg ccgggtccag cttcccgggc aacgactacg cgttcgtccg   960
taccgggggcc ggcgtgaacc tgctggccca ggtcaacaac tactccggtg ccgcgtcca   1020
ggtcgccggg cacaccgcgg ccccgtcgg ctcggccgtg tgccggtccg ggtcgaccac   1080
cgggtggcac tgcggcacca tcactgcgct caactcctcg gtcacctacc ccgagggcac   1140
cgtccgcggc ctgatccgca ccaccgtctg cgccgagccc ggcgactccg gtggctcgct   1200

```
gctcgccggc aaccaggccc agggcgtcac gtccggcggc tccggcaact gccgcaccgg    1260
tggcaccacg ttcttccagc cggtcaaccc catcctccag gcgtacggcc tgaggatgat    1320
caccacggac tcgggcagca gcccggcccc tgcaccgacc tcctgcaccg gctacgcccg    1380
caccttcacc gggaccctcg cggccggccg ggccgccgcc cagcccaacg ggtcctacgt    1440
gcaggtcaac cggtccggga cccacagcgt gtgcctcaac gggccctccg gtgcggactt    1500
cgacctctac gtgcagcgct ggaacggcag ctcctgggtg accgtcgccc agagcacctc    1560
ccccggctcc aacgagacca tcacctaccg cggcaacgcc ggctactacc gctacgtggt    1620
caacgccgcg tccggctccg gtgcctacac catggggctc accctcccct gacgtagcgc    1680
```

<210>   2
<211>   1488
<212>   DNA
<213>   Cellulomonas strain 69B4

<400>   2
```
atgacaccac gcacagtcac gcgggccctg gccgtggcca ccgcagccgc cacactcctg      60
gcaggcggca tggccgccca ggccaacgag cccgcaccac ccgggagcgc gagcgcaccg     120
ccacgcctgg ccgagaagct cgaccccgac ctcctcgagg ccatggagcg cgacctgggc     180
ctcgacgcgg aggaagccgc cgccaccctg gcgttccagc acgacgcagc cgagaccggc     240
gaggccctcg ccgaagagct cgacgaggac ttcgccggca cctgggtcga ggacgacgtc     300
ctgtacgtcg ccaccaccga cgaggacgcc gtcgaggagg tcgagggcga aggcgccacg     360
gccgtcaccg tcgagcactc cctggccgac ctcgaggcct ggaagaccgt cctcgacgcc     420
gccctcgagg ccacgacga cgtgcccacc tggtacgtcg acgtcccgac caacagcgtc      480
gtcgtcgccg tcaaggccgg agcccaggac gtcgccgccg cctcgtcga aggtgccgac      540
gtcccgtccg acgccgtgac cttcgtcgag accgacgaga ccccgcggac catgttcgac     600
gtgatcggcg gcaacgccta caccatcggg gggcgcagcc gctgctcgat cgggttcgcg     660
gtcaacggcg ggttcatcac cgccggccac tgcggccgca ccggcgccac caccgccaac     720
cccaccggga ccttcgccgg gtccagcttc ccgggcaacg actacgcgtt cgtccgtacc     780
ggggccggcg tgaacctgct ggcccaggtc aacaactact ccggtggccg cgtccaggtc     840
gccgggcaca ccgcggcccc cgtcggctcg gccgtgtgcc ggtccgggtc gaccaccggg     900
tggcactgcg gcaccatcac tgcgctcaac tcctcggtca cctaccccga gggcaccgtc     960
cgcggcctga tccgcaccac cgtctgcgcc gagcccggcg actccggtgg ctcgctgctc    1020
gccggcaacc aggcccaggg cgtcacgtcc ggcggctccg gcaactgccg caccggtggc    1080
accacgttct tccagccggt caaccccatc ctccaggcgt acggcctgag gatgatcacc    1140
acggactcgg gcagcagccc ggccctgca ccgacctcct gcaccggcta cgcccgcacc    1200
ttcaccggga ccctcgcggc cggccgggcc gccgcccagc caacgggtc ctacgtgcag     1260
gtcaaccggt ccgggaccca gagcgtgtgc ctcaacgggc cctccggtgc ggacttcgac    1320
ctctacgtgc agcgctggaa cggcagctcc tgggtgaccg tcgcccagag cacctccccc    1380
ggctccaacg agaccatcac ctaccgcggc aacgccggct actaccgcta cgtggtcaac    1440
gccgcgtccg gctccggtgc ctacaccatg gggctcaccc tccctga              1488
```

<210>   3
<211>   1404
<212>   DNA
<213>   Cellulomonas spp.

<400>   3
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aacgagcccg caccacccgg gagcgcgagc gcaccgccac gcctggccga gaagctcgac      60
cccgacctcc tcgaggccat ggagcgcgac ctgggcctcg acgcggagga agccgccgcc     120
accctggcgt tccagcacga cgcagccgag accggcgagg ccctcgccga agagctcgac     180
gaggacttcg ccggcacctg ggtcgaggac gacgtcctgt acgtcgccac caccgacgag     240
gacgccgtcg aggaggtcga gggcgaaggc gccacggccg tcaccgtcga gcactccctg     300
gccgacctcg aggcctggaa gaccgtcctc gacgccgccc tcgagggcca cgacgacgtg     360
cccacctggt acgtcgacgt cccgaccaac agcgtcgtcg tcgccgtcaa ggccggagcc     420
caggacgtcg ccgccggcct cgtcgaaggt gccgacgtcc cgtccgacgc cgtgaccttc     480
gtcgagaccg acgagacccc gcggaccatg ttcgacgtga tcggcggcaa cgcctacacc     540
atcgggggc gcagccgctg ctcgatcggg ttcgcggtca acggcgggtt catcaccgcc     600
```

```
ggccactgcg gccgcaccgg cgccaccacc gccaacccca ccgggacctt cgccgggtcc     660
agcttcccgg gcaacgacta cgcgttcgtc cgtaccgggg ccggcgtgaa cctgctggcc     720
caggtcaaca actactccgg tggccgcgtc caggtcgccg ggcacaccgc ggcccccgtc     780
ggctcggccg tgtgccggtc cgggtcgacc accgggtggc actgcggcac catcactgcg     840
ctcaactcct cggtcaccta ccccgagggc accgtccgcg gcctgatccg caccaccgtc     900
tgcgccgagc ccggcgactc cggtggctcg ctgctcgccg gcaaccaggc ccagggcgtc     960
acgtccggcg gctccggcaa ctgccgcacc ggtggcacca cgttcttcca gccggtcaac    1020
cccatcctcc aggcgtacgg cctgaggatg atcaccacgg actcgggcag cagcccggcc    1080
cctgcaccga cctcctgcac cggctacgcc cgcaccttca ccgggaccct cgcggccggc    1140
cgggccgccg cccagcccaa cgggtcctac gtgcaggtca accggtccgg acccacagc     1200
gtgtgcctca acgggccctc cggtgcggac ttcgacctct acgtgcagcg ctggaacggc    1260
agctcctggg tgaccgtcgc ccagagcacc tcccccggct ccaacgagac catcacctac    1320
cgcggcaacg ccggctacta ccgctacgtg gtcaacgccg gtccggctc cggtgcctac     1380
accatggggc tcaccctccc ctga                                          1404


<210>  4
<211>  567
<212>  DNA
<213>  Cellulomonas spp.


<400>  4
ttcgacgtga tcggcggcaa cgcctacacc atcggggggc gcagccgctg ctcgatcggg      60
ttcgcggtca acggcgggtt catcaccgcc ggccactgcg gccgcaccgg cgccaccacc     120
gccaacccca ccgggacctt cgccgggtcc agcttcccgg gcaacgacta cgcgttcgtc     180
cgtaccgggg ccggcgtgaa cctgctggcc caggtcaaca actactccgg tggccgcgtc     240
caggtcgccg ggcacaccgc ggcccccgtc ggctcggccg tgtgccggtc cgggtcgacc     300
accgggtggc actgcggcac catcactgcg ctcaactcct cggtcaccta ccccgagggc     360
accgtccgcg gcctgatccg caccaccgtc tgcgccgagc ccggcgactc cggtggctcg     420
ctgctcgccg gcaaccaggc ccagggcgtc acgtccggcg gctccggcaa ctgccgcacc     480
ggtggcacca cgttcttcca gccggtcaac cccatcctcc aggcgtacgg cctgaggatg     540
atcaccacgg actcgggcag cagcccg                                         567


<210>  5
<211>  83
<212>  DNA
<213>  Cellulomonas strain 69B4


<400>  5
atgacaccac cacagtcacg cgggccctgg ccgtggccac cgcagccgcc acactcctgg      60
caggcggcat ggccgcccag gcc                                             83


<210>  6
<211>  495
<212>  PRT
<213>  Cellulomonas strain 69B4


<400>  6


Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1               5                   10                  15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala
            20                  25                  30
Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys Leu Asp
        35                  40                  45
Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp Ala Glu
    50                  55                  60
Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu Thr Gly
```

Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val
                    85   90   95
Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala Val Glu
                    100   105   110
Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His Ser Leu
        115   120   125
Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu Glu Gly
        130   135   140
His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn Ser Val
145   150   155   160
Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly Leu Val
                    165   170   175
Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu Thr Asp
                    180   185   190
Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
            195   200   205
Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn Gly Gly
        210   215   220
Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn
225   230   235   240
Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
                    245   250   255
Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val Asn Asn
                    260   265   270
Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala Pro Val
            275   280   285
Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
        290   295   300
Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly Thr Val
305   310   315   320
Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
                    325   330   335
Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly
            340   345   350
Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Asn
            355   360   365
Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp Ser Gly
        370   375   380
Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly Tyr Ala Arg Thr
385   390   395   400
Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala Gln Pro Asn Gly
                    405   410   415
Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser Val Cys Leu Asn
                    420   425   430
Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln Arg Trp Asn Gly
        435   440   445
Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro Gly Ser Asn Glu
        450   455   460
Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn
465   470   475   480
Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro
                    485   490   495

<210>   7
<211>   467
<212>   PRT

<213> Cellulomonas strain 69B4

<400> 7

```
Asn Glu Pro Ala Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala
1               5                   10                  15
Glu Lys Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly
            20                  25                  30
Leu Asp Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala
        35                  40                  45
Ala Glu Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala
    50                  55                  60
Gly Thr Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu
65                  70                  75                  80
Asp Ala Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val
                85                  90                  95
Glu His Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala
            100                 105                 110
Ala Leu Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro
            115                 120                 125
Thr Asn Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala
        130                 135                 140
Ala Gly Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe
145                 150                 155                 160
Val Glu Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly
                165                 170                 175
Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala
            180                 185                 190
Val Asn Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala
            195                 200                 205
Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly
        210                 215                 220
Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
225                 230                 235                 240
Gln Val Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr
                245                 250                 255
Ala Ala Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly
            260                 265                 270
Trp His Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro
            275                 280                 285
Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro
    290                 295                 300
Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val
305                 310                 315                 320
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe
                325                 330                 335
Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr
            340                 345                 350
Thr Asp Ser Gly Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly
        355                 360                 365
Tyr Ala Arg Thr Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala
    370                 375                 380
Gln Pro Asn Gly Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser
385                 390                 395                 400
Val Cys Leu Asn Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln
                405                 410                 415
Arg Trp Asn Gly Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro
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                  420                    425                    430
Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg
        435                    440                    445
Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu
    450                    455                    460
Thr Leu Pro
465


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<213>   Cellulomonas spp.


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Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
1                   5                  10                     15
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
            20                     25                     30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
        35                     40                     45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
    50                     55                     60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
65                     70                     75                 80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
            85                     90                     95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
            100                    105                    110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
        115                    120                    125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
    130                    135                    140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145                    150                    155                160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
                165                    170                    175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
            180                    185


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<212>   PRT
<213>   Cellulomonas strain 69B4


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Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1                   5                  10                     15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
            20                     25


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